

1642

P#21

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/323,597B

DATE: 03/19/2001
 TIME: 10:06:27

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\03192001\I323597B.raw

ENTERED

RECEIVED

MAR 29 2001

TECH CENTER 1600/2900

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4 <110> APPLICANT: Daniel E. Afar
5      Rene S. Hubert
6      Kahan Leong
7      Arthur B. Raitano
8      Douglas C. Saffran
10 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
11      AND THERAPY OF PROSTATE AND COLON CANCER
14 <130> FILE REFERENCE: 129.8USU1
16 <140> CURRENT APPLICATION NUMBER: 09/323,597B
17 <141> CURRENT FILING DATE: 1999-06-01
19 <150> PRIOR APPLICATION NUMBER: 60/087,598
20 <151> PRIOR FILING DATE: 1998-06-01
22 <150> PRIOR APPLICATION NUMBER: 60/091,474
23 <151> PRIOR FILING DATE: 1998-06-29
25 <150> PRIOR APPLICATION NUMBER: 60/129,521
26 <151> PRIOR FILING DATE: 1999-04-14
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30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (112)...(1588)
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43 attgaacatt ccagatacct atcattactc gatgctgttg ataacagcaa g'atg gct      117
44                                     Met Ala
45                                     1
47 ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat      165
48 Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
49      5      10      15
51 gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc      213
52 Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
53      20      25      30
55 act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc      261
56 Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
57      35      40      45      50
59 cag tac gcc ccg agy gtc ctg acg cag gct tcc aac ccc gtc gtc tgc      309
60 Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
61      55      60      65
63 acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag      357
64 Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
65      70      75      80
67 aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct      405
68 Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala

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69	85	90	95	
71	gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc	453		
72	Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser			
73	100	105	110	
75	aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct	501		
76	Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser			
77	115	120	125	130
79	aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat	549		
80	Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn			
81	135	140	145	
83	cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca	597		
84	Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser			
85	150	155	160	
87	tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag	645		
88	Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu			
89	165	170	175	
91	aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt	693		
92	Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe			
93	180	185	190	
95	tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg	741		
96	Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met			
97	195	200	205	210
99	aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac	789		
100	Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr			
101	215	220	225	
103	cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata	837		
104	His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile			
105	230	235	240	
107	gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc	885		
108	Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly			
109	245	250	255	
111	ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac	933		
112	Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His			
113	260	265	270	
115	gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg	981		
116	Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp			
117	275	280	285	290
119	atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg	1029		
120	Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp			
121	295	300	305	
123	cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat	1077		
124	His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr			
125	310	315	320	
127	gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac	1125		
128	Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp			
129	325	330	335	
131	tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct	1173		
132	Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro			
133	340	345	350	

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135 ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc 1221
 136 Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly
 137 355 360 365 370
 139 atg atg ctg cag cca gaa cag ctg tgc tgg att tcc ggg tgg ggg gcc 1269
 140 Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala
 141 375 380 385
 143 acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg 1317
 144 Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val
 145 390 395 400
 147 ctt ctg att gag aca cag aga tgc aac agc aga tat gtc tat gac aac 1365
 148 Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn
 149 405 410 415
 151 ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc 1413
 152 Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val
 153 420 425 430
 155 gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac 1461
 156 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn
 157 435 440 445 450
 159 aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc 1509
 160 Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala
 161 455 460 465
 163 aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac 1557
 164 Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp
 165 470 475 480
 167 tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc 1608
 168 Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
 169 485 490
 171 ttgacgtcgt ttacaagaa aacaatgggg ctgggttttgc ttccccgtgc atgatttact 1668
 172 cttagagatg attcagaggt cacttcattt ttattaaaca gtgaacttgt ctggcaaaaa 1728
 173 aaaaaaaaaa 1738
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 176 <211> LENGTH: 492
 177 <212> TYPE: PRT
 178 <213> ORGANISM: Homo sapiens
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 183 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
 184 20 25 30
 185 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 186 35 40 45
 187 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 188 50 55 60
 189 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 190 65 70 75 80
 191 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 192 85 90 95
 193 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 194 100 105 110

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195 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
196      115      120      125
197 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
198      130      135      140
199 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
200 145      150      155      160
201 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
202      165      170      175
203 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
204      180      185      190
205 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
206      195      200      205
207 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
208      210      215      220
209 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
210 225      230      235      240
211 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
212      245      250      255
213 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
214      260      265      270
215 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
216      275      280      285
217 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
218      290      295      300
219 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
220 305      310      315      320
221 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
222      325      330      335
223 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
224      340      345      350
225 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
226      355      360      365
227 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
228      370      375      380
229 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
230 385      390      395      400
231 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
232      405      410      415
233 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
234      420      425      430
235 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
236      435      440      445
237 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
238      450      455      460
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240 465      470      475      480
241 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
242      485      490
244 <210> SEQ ID NO: 3

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Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03192001\I323597B.raw

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252 cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc      155
253 ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg      203
254 ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc      251
255 tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act      299
256 aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctg gtc gga      347
257 gct gcg ctg gcc gct ggc cta ctg tgg aag ttc atg ggc agc aag tgc      395
258 tcc aac tct ggg cga ata gag tgc tcc tca ggt acc tgc atc aac ccc      443
259 tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag      491
260 aat cgg tgt gtt cgc ctg tac gga cca aac ttc atc ctt cag atg tac      539
261 tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac      587
262 gag aac tac ggg cgg gcc ggc atg agg gac atg ggc tat aag aat aat      635
263 ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt      683
264 atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg      731
265 tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt      779
266 tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg      827
267 ggc ggt gag agc gcg ctg ccg ggg gcc tgg ccc tgg cag gtc agc ctg      875
268 cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag      923
269 tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca      971
270 tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc      1019
271 tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat      1067
272 gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag      1115
273 cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca      1163
274 ggc atg atg ctg cag cca gaa cag ctg tgc tgg att tcc ggg tgg ggg      1211
275 gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag      1259
276 gtg ctt ctg att gag aca cag aga tgc aac agc aga tat gtc tat gac      1307
277 aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac      1355
278 gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tgg aac      1403
279 aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt      1451
280 gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg      1499
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282 gtcttcgtcc ttgacgtcgt ttacaagaa aacaatgggg ctgggttttg tccccgtgc      1603
283 atgatttact cttagagatg attcagaggt cacttcattt ttattaaaca gtgaacttgt      1663
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286 attgtggaag gaagaggggt ggagggtgcc cccattgaga tcttctgtgt ggtcctttc      1843
287 caggggccaa ttttgatga gcatggagct gtcacttctc agctgctgga tgacttgaga      1903
288 tgaaaaagga gagacatgga aagggagaca gccaggtggc acctgcagcg gctgccctct      1963
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291 acgtggtagt cacttgtaag ggaacagaa acatttttgt tcttatgggg tgagaatata      2143
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293 gcaggtctcc acctgcacat tgggtggggc tcttgggagg gagactcagc ctctctctc      2263
294 atctccctc accctgctcc tagcacctg gagagtgaat gcccttgtgt ccttggcagg      2323

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VERIFICATION SUMMARY
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Input Set : A:\Seqlist.txt
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L:168 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5